

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/769,218
Source: EFW16
Date Processed by STIC: 4/5/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/05/2006

PATENT APPLICATION: US/10/769,218

TIME: 10:20:07

Input Set : E:\Princeton 151 Sequence Listing.txt

Output Set: N:\CRF4\04052006\J769218.raw

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3 <110> APPLICANT: Shi, Yigong
5 <120> TITLE OF INVENTION: CASPASE-9:BIR DOMAIN OF XIAP COMPLEXES AND METHODS OF USE
7 <130> FILE REFERENCE: 112911.01501
9 <140> CURRENT APPLICATION NUMBER: 10/769,218
10 <141> CURRENT FILING DATE: 2004-01-30
12 <150> PRIOR APPLICATION NUMBER: 60/443,590
13 <151> PRIOR FILING DATE: 2003-01-30
15 <160> NUMBER OF SEQ ID NOS: 23
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 277
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
26 Gly Ala Leu Glu Ser Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu
27 1 5 10 15
30 Ser Met Glu Pro Cys Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe
31 20 25 30
34 Cys Arg Glu Ser Gly Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys
35 35 40 45
38 Glu Lys Leu Arg Arg Arg Phe Ser Ser Leu His Phe Met Val Glu Val
39 50 55 60
42 Lys Gly Asp Leu Thr Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu
43 65 70 75 80
46 Ala Arg Gln Asp His Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu
47 85 90 95
50 Ser His Gly Cys Gln Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr
51 100 105 110
54 Gly Thr Asp Gly Cys Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe
55 115 120 125
58 Asn Gly Thr Ser Cys Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe
59 130 135 140
62 Ile Gln Ala Cys Gly Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala
63 145 150 155 160
66 Ser Thr Ser Pro Glu Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp
67 165 170 175
70 Ala Thr Pro Phe Gln Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala
71 180 185 190
74 Ile Ser Ser Leu Pro Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr
75 195 200 205
78 Phe Pro Gly Phe Val Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr
79 210 215 220
82 Val Glu Thr Leu Asp Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp

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83 225                230                235                240
86 Leu Gln Ser Leu Leu Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly
87                245                250                255
90 Ile Tyr Lys Gln Met Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu
91                260                265                270
94 Phe Phe Lys Thr Ser
95                275
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 98
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
105 Ser Thr Asn Leu Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg
106 1                5                10                15
109 Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu
110                20                25                30
113 Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys
114                35                40                45
117 Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro
118 50                55                60
121 Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu
122 65                70                75                80
125 Gln Lys Gly Gln Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser Leu
126                85                90                95
129 Glu Glu
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 416
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
140 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
141 1                5                10                15
144 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Ala Leu Leu Ser Arg
145                20                25                30
148 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
149                35                40                45
152 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
153 50                55                60
156 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
157 65                70                75                80
160 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Ala
161                85                90                95
164 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
165                100                105                110
168 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
169                115                120                125
172 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
173 130                135                140
176 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys

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177 145          150          155          160
180 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
181          165          170          175
184 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
185          180          185          190
188 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
189          195          200          205
192 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
193          210          215          220
196 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
197 225          230          235          240
200 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
201          245          250          255
204 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
205          260          265          270
208 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
209          275          280          285
212 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
213          290          295          300
216 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
217 305          310          315          320
220 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
221          325          330          335
224 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
225          340          345          350
228 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
229          355          360          365
232 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
233          370          375          380
236 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
237 385          390          395          400
240 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
241          405          410          415
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 98
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 4
251 Ser Thr Asn Leu Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg
252 1          5          10          15
255 Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu
256          20          25          30
259 Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys
260          35          40          45
263 Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro
264          50          55          60
267 Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu
268 65          70          75          80
271 Gln Lys Gly Gln Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser Leu

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272                85                90                95
275 Glu Glu
279 <210> SEQ ID NO: 5
280 <211> LENGTH: 416
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 5
286 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
287 1                5                10                15
290 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Ala Leu Leu Ser Arg
291                20                25                30
294 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
295                35                40                45
298 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
299                50                55                60
302 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
303 65                70                75                80
306 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Ala
307                85                90                95
310 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
311                100               105               110
314 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
315                115               120               125
318 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
319                130               135               140
322 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
323 145               150               155               160
326 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
327                165               170               175
330 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
331                180               185               190
334 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
335                195               200               205
338 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
339                210               215               220
342 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
343 225               230               235               240
346 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
347                245               250               255
350 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
351                260               265               270
354 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
355                275               280               285
358 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
359                290               295               300
362 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
363 305               310               315               320
366 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
367                325               330               335

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370 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
371          340          345          350
374 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
375          355          360          365
378 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
379          370          375          380
382 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
383 385          390          395          400
386 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
387          405          410          415
390 <210> SEQ ID NO: 6
391 <211> LENGTH: 416
392 <212> TYPE: PRT
393 <213> ORGANISM: Homo sapiens
395 <400> SEQUENCE: 6
397 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
398 1          5          10          15
401 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Ala Leu Leu Ser Arg
402          20          25          30
405 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
406          35          40          45
409 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
410          50          55          60
413 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
414 65          70          75          80
417 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Ala
418          85          90          95
421 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
422          100          105          110
425 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
426          115          120          125
429 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
430          130          135          140
433 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
434 145          150          155          160
437 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
438          165          170          175
441 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
442          180          185          190
445 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
446          195          200          205
449 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
450          210          215          220
453 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
454 225          230          235          240
457 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
458          245          250          255
461 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
462          260          265          270

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VERIFICATION SUMMARY

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Input Set : E:\Princeton 151 Sequence Listing.txt

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